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SEQUENCE LISTING

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<120> GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY

<130> 001560-377

<140> US 09/446,089
<141> 1999-12-17

<150> PCT/JP99/02045
<151> 1999-04-16

<150> JP 10/107296
<151> 1998-04-17

<160> 15

<170> PatentIn version 3.0

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<222> (96)..(1781)

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Met Phe Lys Asn Pro Asn
1 5

atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa 161
Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu
10 15 20

tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209
Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
25 30 35

cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 257
Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
40 45 50

ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa 305
Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
55 60 65 70

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tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt      353
Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys
                75                  80                  85

ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc      401
Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser
            90                  95                 100

act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac      449
Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr
        105                 110                 115

att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag      497
Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu
    120                 125                 130

gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac      545
Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr
135                 140                 145                 150

tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa      593
Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln
                155                 160                 165

atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac      641
Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr
            170                 175                 180

ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct      689
Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala
        185                 190                 195

ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca      737
Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser
    200                 205                 210

atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt      785
Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser
215                 220                 225                 230

aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat      833
Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp
                235                 240                 245

tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa      881
Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys
            250                 255                 260

att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc      929
Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe
        265                 270                 275

ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg      977
Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly
    280                 285                 290

tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct     1025
Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser
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295                 300                 305                 310

gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct      1073
Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala
                315                 320                 325

aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg      1121
Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp
            330                 335                 340

tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat      1169
Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp
        345                 350                 355

cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag      1217
Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu
    360                 365                 370

atg gtt cgg gtc aag gtt cgg gat tgc tta gat gaa aag aaa cta ggg      1265
Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly
375                 380                 385                 390

tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca      1313
Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr
                395                 400                 405

cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act      1361
Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr
            410                 415                 420

gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa      1409
Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys
        425                 430                 435

gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac      1457
Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp
    440                 445                 450

gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac      1505
Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp
455                 460                 465                 470

cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac      1553
His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp
                475                 480                 485

ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg      1601
Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val
            490                 495                 500

agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta      1649
Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu
        505                 510                 515

tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa      1697
Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu
    520                 525                 530
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gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg      1745
Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala
535                 540                 545                 550

atc aag att cat aat gtc aag att gag ctt gat ggc taataaattc          1791
Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly
                555                 560

tattgatttc ttctcaacct acagttgatc atttaccgat tgattattcc aataaaagta   1851

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Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn
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Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala
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Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr
65                  70                  75                  80

Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe
                85                  90                  95

Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His
            100                 105                 110

Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu
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Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala
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Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
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Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
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His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
            180                 185                 190

Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
        195                 200                 205

Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
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Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
225                 230                 235                 240

Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln
                245                 250                 255

Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
            260                 265                 270

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
        275                 280                 285

Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
    290                 295                 300

His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
305                 310                 315                 320

Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
                325                 330                 335

Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
            340                 345                 350

Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
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Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
    370                 375                 380
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Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
385 390 395 400

Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
405 410 415

Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile
420 425 430

Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
435 440 445

Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
450 455 460

Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
465 470 475 480

Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
485 490 495

Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
500 505 510

Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
515 520 525

Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
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Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
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Asp Gly

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<400> 4

Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
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<210> 5
<211> 18
<212> PRT
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<400> 5

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Glu Phe

<210> 6
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<220>
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<222> (8)..(8)
<223> Amino acid 8 is Xaa wherein Xaa = unknown or other.

<220>
<221> UNSURE
<222> (28)..(28)
<223> Amino acid 28 is Xaa wherein Xaa = unknown or other.

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Arg Ala Ala His Leu Val Asp Asp Ala Tyr Ile Xaa Lys
20 25

<210> 7
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<400> 7

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Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly Ser Ile Glu
20 25 30

Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser Glu Asn Thr
35 40 45

Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala Arg Asp Pro
50 55 60

Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp Ser Ile Trp
65 70 75 80

Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp Pro Asp Phe
85 90 95

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Val Lys Val Arg Asp Cys Leu Asp Gly Lys Lys Leu Gly
115 120 125

<210> 8
<211> 7
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<213> Artificial Sequence

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<221> PEPTIDE
<222> (2)..(2)
<223> Amino acid 2 is Xaa wherein Xaa = Val or Ile.

<400> 8

Phe Xaa Lys Phe Thr Ala Ile
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<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (6)..(6)
<223> Amino acid 6 is Xaa wherein Xaa = Thr or Pro.

<400> 9

Lys Trp Lys Gly Lys Xaa
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<210> 10
<211> 6
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<400> 10

His Ala Val Cys Asn Glu
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<210> 11
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<221> misc_feature
<222> (6)..(18)
<223> Nucleotides 6, 15 and 18 are "n" wherein "n" = a or c or g or t/u or unknown or other

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<210> 12
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (12)..(12)
<223> Nucleotide 12 is "n" wherein "n" = a or c or g or t/u or unknown or other

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aartggaarg gnaarmc 17

<210> 13
<211> 18
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (4)..(7)
<223> Nucleotides 4 and 7 are "n" wherein "n" = a or c or g or t/u or unknown or other

<400> 13
rtgngcnacr carttytc 18

<210> 14
<211> 20
<212> DNA
<213> Primer

<400> 14
aaggatccgg ccctatcgcc 20

<210> 15
<211> 22
<212> DNA
<213> Primer

<400> 15
gggttcgaag aattcatctc tg 22